

Assignment #11

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Ch24.1

Download the data in the folder dogs and fit some other models, for example using as a predictor the result from the previous trial, or the previous two trials, rather than the total number of shocks and avoidances.

```
options(stringAsFactors = F, max.print = 10000)
setwd("~/Dropbox/WUSTL third/Multilevel Modeling for Quantitative Research/assignment/11")
.libPaths("/Library/Frameworks/R.framework/Versions/3.3/Resources/library")
require(R2jags)
require(rjags)
require(dplyr)
require(magrittr)
dogs_data <- read.table('dogs2.txt', row.names = 1)
y <- dogs_data
n_dogs <- nrow(y)
n_trials <- ncol(y)
```

Part A

Fit this model, as usual building up from simpler versions (first a single- level model, then varying intercepts, then varying slopes, then adding other predictors as appropriate). Plot the data and fitted model to make sure that your model makes sense.

Single Level Model

```

dogs_1 <- function() {
  for (j in 1:n_dogs) {
    prel_s[j, 1] <- 0
    prel_a[j, 1] <- 0
    for (t in 2:n_trials) {
      prel_s[j, t] <- y[j, t-1]
      prel_a[j, t] <- 1 - y[j, t-1]
    }
    for (t in 1:n_trials) {
      y[j, t] ~ dbin(p[j, t], 1)
      log(p[j, t]) <- b_s * prel_s[j, t] + b_a * prel_a[j, t]
    }
  }
  b_s <- -b_s_neg
  b_a <- -b_a_neg
  b_s_neg ~ dlnorm(mu_b_s, tau_b_s)
  b_a_neg ~ dlnorm(mu_b_a, tau_b_a)
  tau_b_s <- pow(sigma_b_s, -2)
  tau_b_a <- pow(sigma_b_a, -2)

  mu_b_s ~ dnorm(0, .0001)
  mu_b_a ~ dnorm(0, .0001)
  sigma_b_s ~ dunif(0, 100)
  sigma_b_a ~ dunif(0, 100)
}

data_1 <- list("y", "n_dogs", "n_trials")
inits_1 <- function (){
  list(b_s_neg=rlnorm(1),
       b_a_neg=rlnorm(1),
       mu_b_s= rnorm(1),
       mu_b_a=rnorm(1),
       sigma_b_s=dunif(1, 0, 100),
       sigma_b_a=dunif(1, 0, 100))
}
params_1 <- c ('b_s', 'b_a')

dogs_1_jags <- jags(data_1, inits_1, params_1, n.chains = 3, n.iter = 1000, dogs_1)
plot(dogs_1_jags)
dogs_1_jags$BUGSoutput

```

Output

```

Inference for Bugs model at "/var/folders/ld/tp92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMtZ
Z/model520c23f95225.txt", fit using jags,
  3 chains, each with 1000 iterations (first 500 discarded)
  n.sims = 1500 iterations saved
      mean sd 2.5% 25% 50% 75% 97.5% Rhat n.eff
b_a      -2.0 0.1 -2.2 -2.0 -1.9 -1.9 -1.7    1 1500
b_s      -0.5 0.1 -0.7 -0.6 -0.5 -0.5 -0.4    1  580
deviance 716.7 2.1 714.6 715.1 716.1 717.6 722.0    1 1500

```

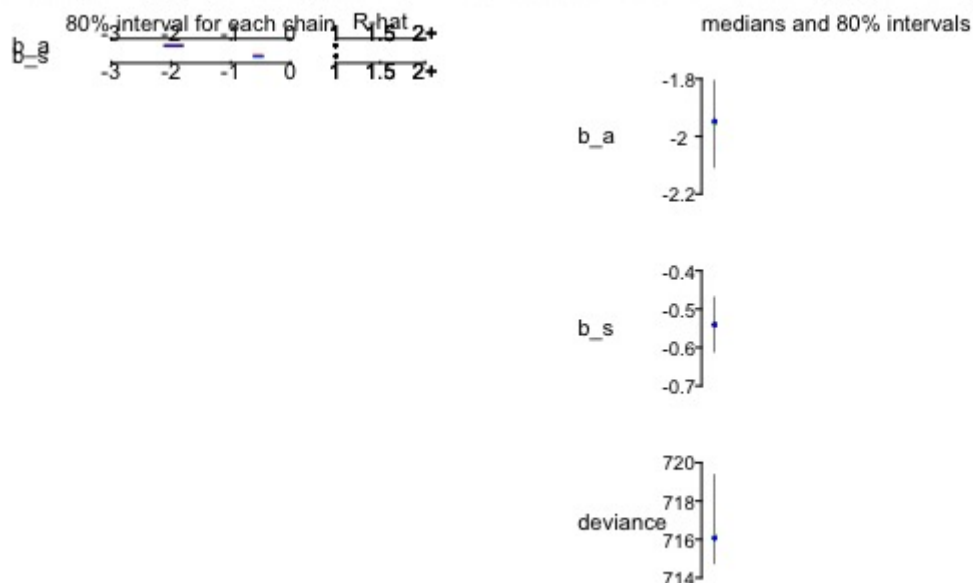
For each parameter, n.eff is a crude measure of effective sample size, and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule, $pD = \text{var}(\text{deviance})/2$)

$pD = 2.1$ and $DIC = 718.8$

DIC is an estimate of expected predictive error (lower deviance is better).

92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMtZ/model520c23f95225.txt", fit using jags, 3 chains, each with 100



Based on this single lever model, both of the shock (slope = -0.5) and the avoid (slope = -2.0) of the previous trials decrease the possibility of shock and the avoid plays a more important role compared to the shock.

Varying Intercept Model

```

dogs_2 <- function() {
  for (j in 1:n_dogs) {
    prel_s[j, 1] <- 0
    prel_a[j, 1] <- 0
    for (t in 2:n_trials) {
      prel_s[j, t] <- y[j, t-1]
      prel_a[j, t] <- 1 - y[j, t-1]
    }
    for (t in 1:n_trials) {
      y[j, t] ~ dbin(p[j, t], 1)
      logit(p[j, t]) <- b_s * prel_s[j, t] + b_a * prel_a[j, t] + b0[j]
    }
    b0[j] ~ dnorm(mu_b0, tau_b0)
  }
  mu_b0 ~ dnorm(0, .0001)
  tau_b0 <- pow(sigma_b0, -2)
  sigma_b0 ~ dunif(0, 100)

  b_s ~ dnorm(mu_b_s, tau_b_s)
  b_a ~ dnorm(mu_b_a, tau_b_a)
  tau_b_s <- pow(sigma_b_s, -2)
  tau_b_a <- pow(sigma_b_a, -2)
  mu_b_s ~ dnorm(0, .0001)
  mu_b_a ~ dnorm(0, .0001)
  sigma_b_s ~ dunif(0, 100)
  sigma_b_a ~ dunif(0, 100)
}

data_2 <- list("y", "n_dogs", "n_trials")
inits_2 <- function () {
  list(b_s=rnorm(1),
       b_a=rnorm(1),
       mu_b_s= rnorm(1),
       mu_b_a=rnorm(1),
       sigma_b_s=dunif(1, 0, 100),
       sigma_b_a=dunif(1, 0, 100),
       b0=rnorm(n_dogs),
       mu_b0=rnorm(1),
       sigma_b0=runif(1, 0, 100))
}
params_2 <- c ('b_s', 'b_a', 'b0')

dogs_2_jags <- jags(data_2, inits_2, params_2, n.chains = 3, n.iter = 5000, dogs_2)\

plot(dogs_2_jags)
dogs_2_jags$BUGSoutput

```

Output

```

Inference for Bugs model at "/var/folders/ld/tp92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMTz
Z/model520c4afa0c00.txt", fit using jags,
  3 chains, each with 5000 iterations (first 2500 discarded), n.thin = 2
n.sims = 3750 iterations saved

```

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
b0[1]	7.7	2.4	3.4	5.1	8.5	9.3	11.2	5.1	3
b0[2]	7.7	2.4	3.4	5.1	8.6	9.3	11.3	5.1	3
b0[3]	7.7	2.4	3.4	5.1	8.5	9.3	11.3	5.1	3
b0[4]	7.7	2.4	3.4	5.1	8.5	9.3	11.2	5.1	3
b0[5]	7.7	2.4	3.4	5.1	8.5	9.3	11.2	5.1	3
...									
b0[25]	7.7	2.4	3.3	5.1	8.5	9.3	11.2	5.1	3
b0[26]	7.7	2.4	3.3	5.1	8.5	9.3	11.2	5.1	3
b0[27]	7.7	2.4	3.3	5.1	8.5	9.3	11.2	5.1	3
b0[28]	7.7	2.4	3.4	5.1	8.5	9.3	11.2	5.1	3
b0[29]	7.7	2.4	3.4	5.1	8.5	9.3	11.2	5.1	3
b0[30]	7.7	2.4	3.3	5.1	8.5	9.3	11.2	5.1	3
b_a	-9.5	2.4	-13.0	-11.1	-10.3	-6.9	-5.2	4.7	3
b_s	-7.4	2.4	-10.9	-9.0	-8.2	-4.8	-3.1	4.7	3
deviance	716.8	2.9	711.9	715.0	716.3	718.1	723.7	1.0	170

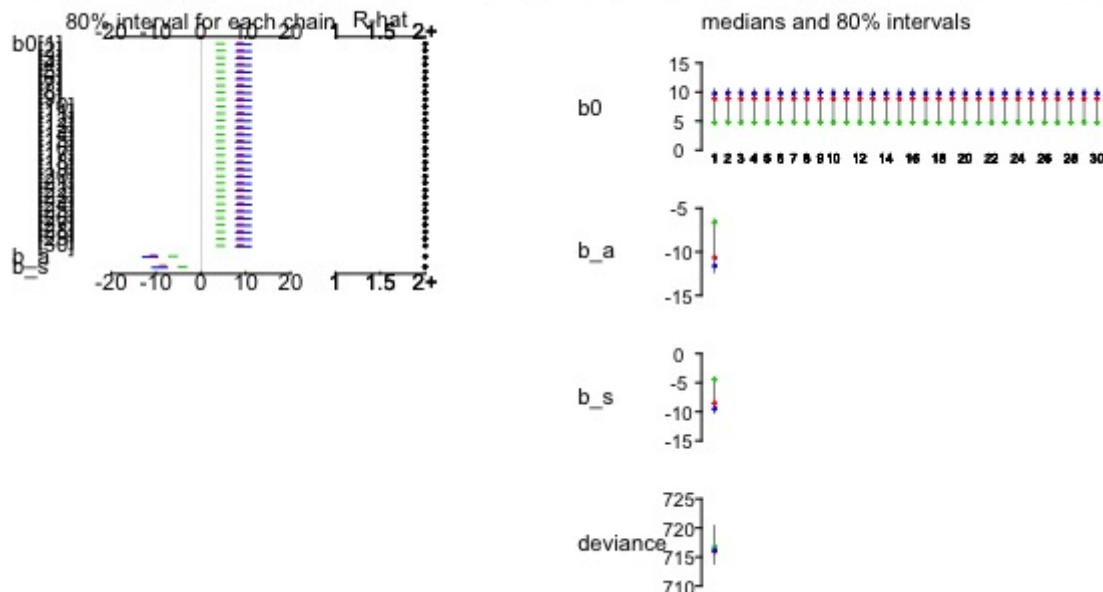
For each parameter, n.eff is a crude measure of effective sample size, and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule, $pD = \text{var}(\text{deviance})/2$)

$pD = 4.1$ and $DIC = 720.8$

DIC is an estimate of expected predictive error (lower deviance is better).

32rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMTzZ/model520c4afa0c00.txt", fit using jags, 3 chains, each with 5000



Based on this varying intercept model, both of the shock (slope = -7.4) and the avoid (slope = -9.5) of the previous trials decrease the possibility of shock and the avoid plays a more important role compared to the shock. The varying intercepts doesn't change much among different dogs.

Varying Slopes Model

```

dogs_3 <- function() {
  for (j in 1:n_dogs) {
    prel_s[j, 1] <- 0
    prel_a[j, 1] <- 0
    for (t in 2:n_trials) {
      prel_s[j, t] <- y[j, t-1]
      prel_a[j, t] <- 1 - y[j, t-1]
    }
    for (t in 1:n_trials) {
      y[j, t] ~ dbin(p[j, t], 1)
      log(p[j, t]) <- b_s[j] * prel_s[j, t] + b_a[j] * prel_a[j, t]
    }
    b_s[j] <- -b_s_neg[j]
    b_a[j] <- -b_a_neg[j]
    b_s_neg[j] ~ dlnorm(mu_b_s, tau_b_s)
    b_a_neg[j] ~ dlnorm(mu_b_a, tau_b_a)
  }
  tau_b_s <- pow(sigma_b_s, -2)
  tau_b_a <- pow(sigma_b_a, -2)
  mu_b_s ~ dnorm(0, .0001)
  mu_b_a ~ dnorm(0, .0001)
  sigma_b_s ~ dunif(0, 100)
  sigma_b_a ~ dunif(0, 100)
}

data_3 <- list("y", "n_dogs", "n_trials")
inits_3 <- function (){
  list(b_s_neg=rlnorm(n_dogs),
       b_a_neg=rlnorm(n_dogs),
       mu_b_s= rnorm(1),
       mu_b_a=rnorm(1),
       sigma_b_s=dunif(1, 0, 100),
       sigma_b_a=dunif(1, 0, 100))
}
params_3 <- c ('b_s', 'b_a')

dogs_3_jags <- jags(data_3, inits_3, params_3, n.chains = 3, n.iter = 1000, dogs_3)

plot(dogs_3_jags)
dogs_3_jags$BUGSoutput

```

Output

Inference for Bugs model at `"/var/folders/ld/tp92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMTzZ/model520c45800d96.txt"`, fit using jags,

3 chains, each with 1000 iterations (first 500 discarded)

n.sims = 1500 iterations saved

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
b_a[1]	-2.0	0.4	-3.1	-2.2	-1.9	-1.9	-1.5	1.1	27
b_a[2]	-2.0	0.4	-3.0	-2.2	-1.9	-1.9	-1.4	1.1	27
b_a[3]	-1.8	0.3	-2.4	-1.9	-1.8	-1.6	-1.1	1.1	44
b_a[4]	-1.8	0.2	-2.3	-1.9	-1.9	-1.7	-1.3	1.1	62
b_a[5]	-2.3	0.6	-4.0	-2.5	-2.1	-1.9	-1.7	1.3	11
...									
b_a[25]	-1.9	0.3	-2.5	-2.0	-1.9	-1.7	-1.3	1.1	370
b_a[26]	-1.9	0.3	-2.6	-2.0	-1.9	-1.8	-1.4	1.1	240
b_a[27]	-2.2	0.5	-3.3	-2.3	-2.0	-1.9	-1.6	1.2	14
b_a[28]	-1.8	0.3	-2.4	-1.9	-1.9	-1.7	-1.2	1.1	86
b_a[29]	-1.7	0.3	-2.2	-1.9	-1.8	-1.5	-1.1	1.2	17
b_a[30]	-2.0	0.3	-2.8	-2.2	-1.9	-1.8	-1.5	1.1	41
b_s[1]	-0.7	0.3	-1.5	-0.9	-0.7	-0.5	-0.3	1.0	690
b_s[2]	-0.4	0.1	-0.7	-0.5	-0.4	-0.3	-0.2	1.0	53
b_s[3]	-0.6	0.2	-1.1	-0.7	-0.6	-0.5	-0.3	1.0	260
b_s[4]	-0.8	0.4	-1.8	-1.0	-0.7	-0.6	-0.4	1.0	140
b_s[5]	-0.4	0.2	-0.8	-0.5	-0.4	-0.3	-0.2	1.0	84
...									
b_s[25]	-0.6	0.2	-1.0	-0.7	-0.6	-0.5	-0.3	1.0	230
b_s[26]	-0.8	0.3	-1.6	-0.9	-0.7	-0.6	-0.4	1.0	310
b_s[27]	-0.6	0.2	-1.0	-0.7	-0.5	-0.4	-0.3	1.0	460
b_s[28]	-0.8	0.3	-1.5	-0.9	-0.7	-0.6	-0.4	1.0	1500
b_s[29]	-0.7	0.2	-1.2	-0.8	-0.6	-0.5	-0.3	1.0	890
b_s[30]	-0.6	0.2	-1.2	-0.7	-0.6	-0.5	-0.3	1.0	440
deviance	697.1	10.8	676.1	689.7	697.2	704.9	716.5	1.5	8

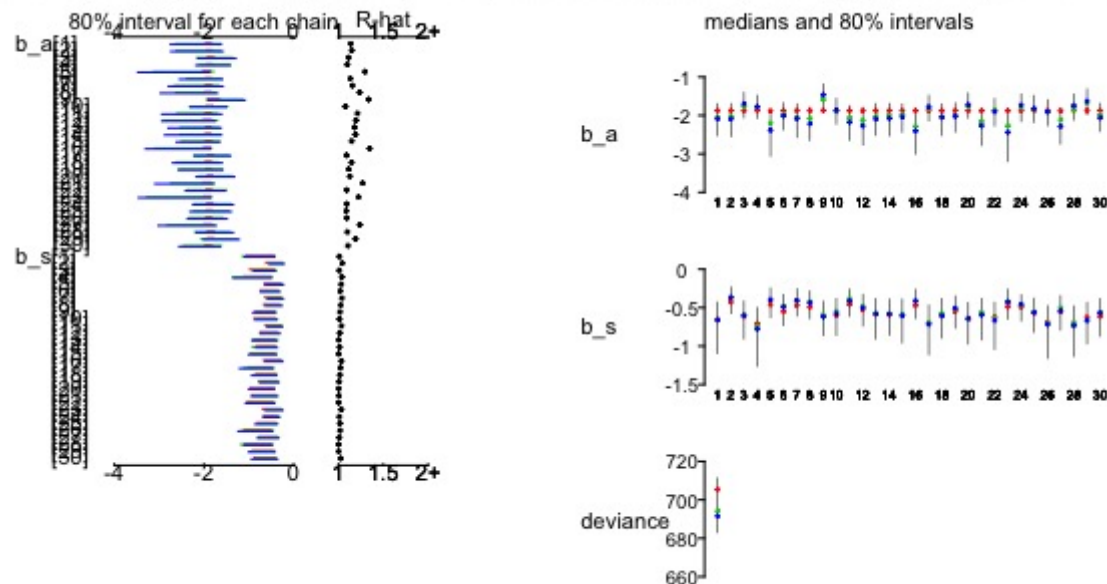
For each parameter, n.eff is a crude measure of effective sample size, and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule, $pD = \text{var}(\text{deviance})/2$)

$pD = 41.2$ and $DIC = 738.3$

DIC is an estimate of expected predictive error (lower deviance is better).

92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMtZ/model520c45800d96.txt", fit using jags, 3 chains, each with 100



Based on this varying slope model, both of the shock (slope = $-0.4 \sim -0.8$) and the avoid (slope = $-1.8 \sim -2.3$) of the previous trials decrease the possibility of shock and the avoid plays a more important role compared to the shock.

Additional Predictor Model


```

# Model_4 (additional predictor)
dogs_4 <- function() {
  for (j in 1:n_dogs) {
    prel_s[j, 1] <- 0
    prel_a[j, 1] <- 0
    pre_num_trials[j, 1] <- 0
    for (t in 2:n_trials) {
      prel_s[j, t] <- y[j, t-1]
      prel_a[j, t] <- 1 - y[j, t-1]
      pre_num_trials[j, t] <- t - 1
    }
    for (t in 1:n_trials) {
      y[j, t] ~ dbin(p[j, t], 1)
      log(p[j, t]) <- b_s[j] * prel_s[j, t] + b_a[j] * prel_a[j, t] + b_n[j] * pre_num_tr
ials[j, t]
    }
    b_n[j] <- -b_n_neg[j]
    b_s[j] <- -b_s_neg[j]
    b_a[j] <- -b_a_neg[j]
    b_n_neg[j] ~ dlnorm(mu_b_n, tau_b_n)
    b_s_neg[j] ~ dlnorm(mu_b_s, tau_b_s)
    b_a_neg[j] ~ dlnorm(mu_b_a, tau_b_a)
  }
  mu_b_n ~ dnorm(0, .0001)
  mu_b_s ~ dnorm(0, .0001)
  mu_b_a ~ dnorm(0, .0001)
  tau_b_n <- pow(sigma_b_n, -2)
  tau_b_s <- pow(sigma_b_s, -2)
  tau_b_a <- pow(sigma_b_a, -2)
  sigma_b_n ~ dunif(0, 100)
  sigma_b_s ~ dunif(0, 100)
  sigma_b_a ~ dunif(0, 100)
}

data_4 <- list("y", "n_dogs", "n_trials")
inits_4 <- function (){
  list(
    b_n_neg=rlnorm(n_dogs),
    b_s_neg=rlnorm(n_dogs),
    b_a_neg=rlnorm(n_dogs),
    mu_b_n= rnorm(1),
    mu_b_s=rnorm(1),
    mu_b_a=rnorm(1),
    sigma_b_n=dunif(1, 0, 100),
    sigma_b_s=dunif(1, 0, 100),
    sigma_b_a=dunif(1, 0, 100))
}
params_4 <- c ('b_s', 'b_a', 'b_n')

dogs_4_jags <- jags(data_4, inits_4, params_4, n.chains = 3, n.iter = 5000, dogs_4)

plot(dogs_4_jags)
dogs_4_jags$BUGSoutput

```

Output

```
Inference for Bugs model at "/var/folders/ld/tp92rb3n3gs4zx9_3_xly5fw0000gn/T//Rtmp1YMTz
Z/model520c16c88927.txt", fit using jags,
  3 chains, each with 5000 iterations (first 2500 discarded), n.thin = 2
n.sims = 3750 iterations saved
```

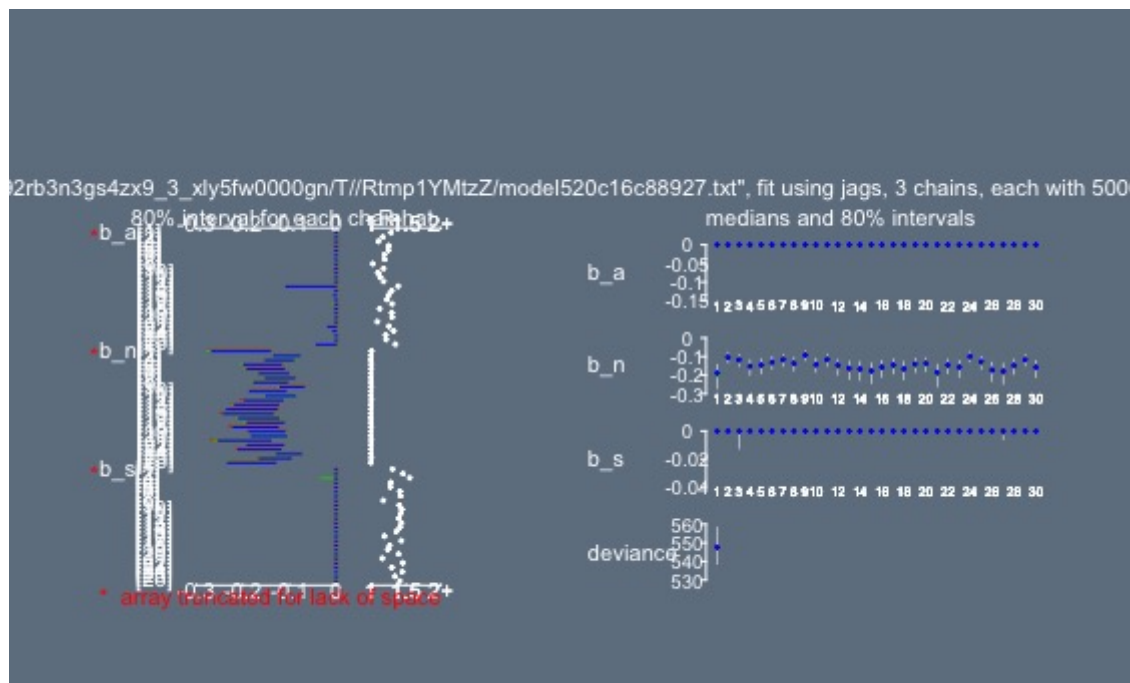
	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
b_a[1]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	73
b_a[2]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	1200
b_a[3]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	550
b_a[4]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	220
b_a[5]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	1400
...									
b_a[25]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	220
b_a[26]	0.0	0.0	-0.1	0.0	0.0	0.0	0.0	1.3	31
b_a[27]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	97
b_a[28]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	70
b_a[29]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	180
b_a[30]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	250
b_n[1]	-0.2	0.1	-0.3	-0.2	-0.2	-0.2	-0.1	1.0	750
b_n[2]	-0.1	0.0	-0.2	-0.1	-0.1	-0.1	-0.1	1.0	1700
b_n[3]	-0.1	0.0	-0.2	-0.1	-0.1	-0.1	-0.1	1.0	3800
b_n[4]	-0.2	0.0	-0.2	-0.2	-0.2	-0.1	-0.1	1.0	2200
b_n[5]	-0.2	0.0	-0.2	-0.2	-0.1	-0.1	-0.1	1.0	3800
...									
b_n[25]	-0.1	0.0	-0.2	-0.1	-0.1	-0.1	-0.1	1.0	530
b_n[26]	-0.2	0.0	-0.3	-0.2	-0.2	-0.1	-0.1	1.0	3800
b_n[27]	-0.2	0.0	-0.3	-0.2	-0.2	-0.2	-0.1	1.0	460
b_n[28]	-0.2	0.0	-0.2	-0.2	-0.1	-0.1	-0.1	1.0	3800
b_n[29]	-0.1	0.0	-0.2	-0.1	-0.1	-0.1	-0.1	1.0	3800
b_n[30]	-0.2	0.0	-0.3	-0.2	-0.2	-0.1	-0.1	1.0	3800
b_s[1]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	52
b_s[2]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	13
b_s[3]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.6	10
b_s[4]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	38
b_s[5]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	16
...									
b_s[25]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.3	18
b_s[26]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	17
b_s[27]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.8	7
b_s[28]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	16
b_s[29]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.4	14
b_s[30]	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	14
deviance	547.9	7.7	534.9	542.4	547.4	552.9	564.4	1.0	2800

For each parameter, n.eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor (at convergence, Rhat=1).

DIC info (using the rule, $pD = \text{var}(\text{deviance})/2$)

$pD = 29.4$ and $DIC = 577.3$

DIC is an estimate of expected predictive error (lower deviance is better).



For this additional predictor model, I add number of trials as a third predictor. After adding this predictor, both of the shock (slope = 0) and the avoid (slope = 0) doesn't matter for this model. However, the number of trials (slope = -0.1 ~ -0.2) plays the most important role.

Part B

Use Bugs to simulate replicated datasets from your model, and make various plots to compare the replicated with the actual data.

Simulation

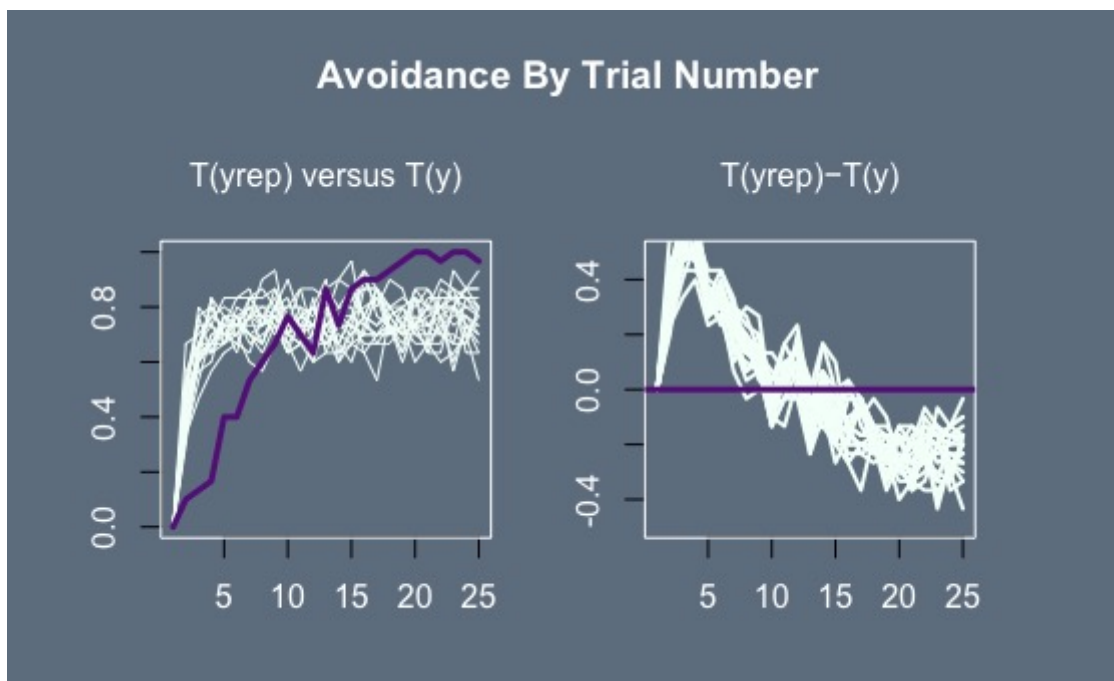
```

b_a <- dogs_3_jags$BUGSoutput$summary[1:30, 1]
b_s <- dogs_3_jags$BUGSoutput$summary[31:60, 1]

n_sims <- 1000
y_rep <- array(NA, c(n_sims, n_dogs, n_trials))
for (j in 1:n_dogs){
  prel_a_rep <- rep (0, n_sims)
  prel_s_rep <- rep (0, n_sims)
  for (t in 1:n_trials){
    p_rep <- exp (b_a[j] * prel_a_rep + b_s[j] * prel_s_rep)
    y_rep[ , j, t] <- rbinom (n_sims, 1, p_rep)
    prel_a_rep <- 1 - y_rep[ , j, t]
    prel_s_rep <- y_rep[ , j, t]
  }
}

par(mfrow=c(1,2),mar=c(2,2,2,2),oma=c(2,2,4,2),col.axis="white",col.main="white",
    col.lab="white",col.sub="white",col="white",bg="slategray")
plot(1:25,1-apply(dogs_data,2,mean),type="n")
rand.sample <- sample(x=1:n_sims,size=20)
for (i in rand.sample) lines(1:25,1-apply(y_rep[i,,],2,mean),col="mintcream")
lines(1:25,1-apply(dogs_data,2,mean),col="darkorchid4",lwd=3,type="l")
mtext(side=3,line=1.25,"T(yrep) versus T(y)")
plot(1:25,seq(-0.5,0.5,length=25),type="n")
for (i in rand.sample)
  lines(1:25,(1-apply(y_rep[i,,],2,mean))-(1-apply(dogs_data,2,mean)),
        col="mintcream",lwd=2,type="l")
abline(h=0,col="darkorchid4",lwd=3)
mtext(side=3,line=1.25,"T(yrep)-T(y)")
title(outer=TRUE,line=2,col="white","Avoidance By Trial Number")

```



I choose to use the varying slope model to do the simulation part. The simulation curves remain much higher than the actual data at the first 10 trials, but lower than the actual data at the last 15 trials, which means this model is not appropriate in predicting the results.

Ch24.4

Model checking for ordered categorical regression:

Part A

Do some simulation-based graphical checking for the ordered logistic regression model that you fit in Exercise 17.11 to the data from the storable-voting experiment.

Model Fit

```

require(R2WinBUGS)
require(R2OpenBUGS)
vote_data <- read.csv('3playergames.csv')

y <- vote_data$vote
x <- vote_data$value
n <- nrow(vote_data)
player <- vote_data$person %>% factor %>% as.numeric
n_cut <- 2
n_player <- player %>% unique %>% length

order_logit <- function() {
  for (i in 1:n) {
    y[i] ~ dcat(P[i, ])
    y_sim[i] ~ dcat(P[i, ])
    P[i, 1] <- 1 - Q[i, 1]
    P[i, 2] <- Q[i, 1] - Q[i, 2]
    P[i, 3] <- Q[i, 2]
    for (k in 1:n_cut) {
      logit(Q[i, k]) <- Z[i, k]
      Z[i, k] <- (x[i] - C[player[i], k])/s[player[i]]
    }
  }
  for (j in 1:n_player) {
    C[j, 1] ~ dnorm(mu_c[1], tau_c[1])
    I(0, C[j, 2])
    C[j, 2] ~ dnorm(mu_c[2], tau_c[2])
    I(C[j, 1], 100)
    s[j] ~ dlnorm(mu_log_s, tau_log_s)
  }
  for (k in 1:n_cut){
    mu_c[k] ~ dnorm(0, 1.E-6)
    I(0, 100)
    tau_c[k] <- pow(sigma_c[k], -2)
    sigma_c[k] ~ dunif(0, 1000)
  }
  mu_log_s ~ dnorm(0, .00001)
  tau_log_s <- pow(sigma_log_s, -2)
  sigma_log_s ~ dunif(0, 1000)
}

data_vote <- list('y', 'x', 'n', 'n_cut', 'n_player', 'player')
C_inits <- array(dim= c(n_player,2))
for (j in 1:n_player){
  for (k in 1:2){
    C_inits[j,k] <- 25+5*k+rnorm(1)
  }
}
inits_vote <- function() {
  list(
    'y_sim'=y,
    "C"=C_inits,
    "s"=rep(10000, n_player),

```

```
"mu_c"=c(20, 80),  
"sigma_c"=runif(n_cut),  
"mu_log_s"=rnorm(1),  
"sigma_log_s"=runif(1)  
)  
}  
  
# write.model(order_logit, 'oder_logit.bug')  
  
params_vote <- c('s', 'C', 'y_sim')  
  
vote_jags_model <- bugs(data_vote, inits_vote, params_vote, order_logit,  
                        n.chains = 3, n.iter = 10000, debug=TRUE)
```

Output

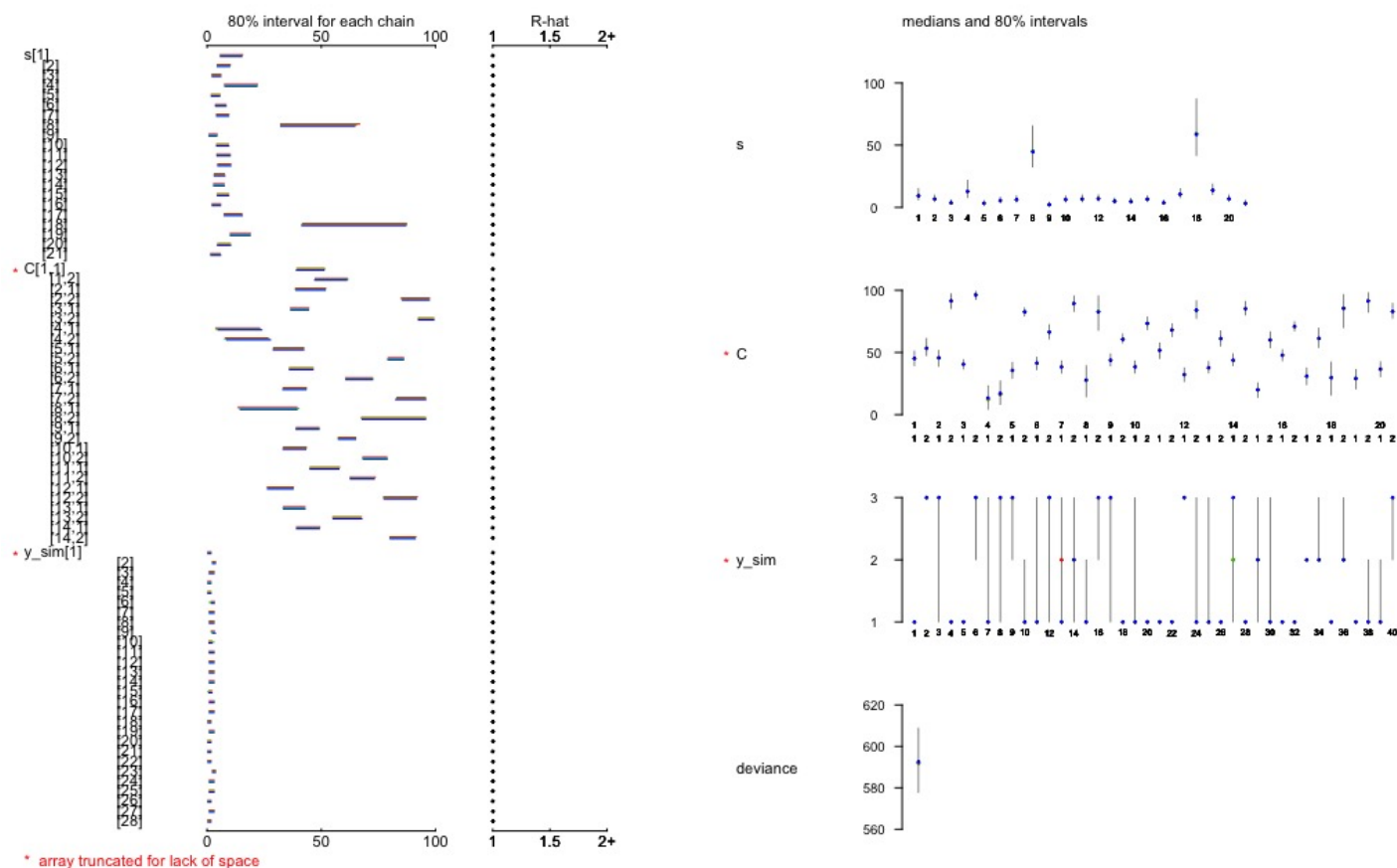
		mean	sd	2.5%	25%	50%	75%	97.5%	
Rhat	n.eff								
s[1]	10.181305	4.36542013	4.6929750	7.30200	9.2710	11.95250	21.490250	1.	
001117	9200								
s[2]	7.067415	2.25927448	3.6509500	5.45875	6.7190	8.31700	12.480250	1.	
001083	11000								
s[3]	3.870234	1.56559758	1.7059500	2.74400	3.5560	4.68200	7.735075	1.	
001350	4400								
s[4]	14.580618	10.84820575	6.0398749	9.82000	12.7550	16.79000	31.430500	1.	
002030	15000								
s[5]	3.546696	1.54022281	1.4149750	2.44500	3.2475	4.33000	7.323100	1.	
001307	4900								
...									
s[15]	6.792026	1.99155116	3.7109750	5.39100	6.5240	7.86525	11.470000	1.	
000927	15000								
s[16]	3.855170	1.49329858	1.7520000	2.78900	3.5950	4.59300	7.493000	1.	
000906	15000								
s[17]	11.084995	3.28194063	6.4710000	8.81475	10.5100	12.72000	19.190250	1.	
000949	15000								
s[18]	62.342048	19.45617618	34.9800000	48.81750	58.9400	71.86000	110.200000	1.	
001085	11000								
s[19]	14.264241	3.47929161	8.8369250	11.77000	13.8000	16.27000	22.330000	1.	
000941	15000								
s[20]	7.201995	2.24216548	3.8449500	5.61875	6.8525	8.40350	12.570250	1.	
000968	15000								
s[21]	3.492759	1.71594086	1.1250000	2.26400	3.1640	4.35025	7.808075	1.	
000949	15000								
C[1,1]	45.271927	4.80034424	35.7397500	42.18000	45.2500	48.31000	54.830250	1.	
001363	4300								
C[1,2]	54.041903	5.78309925	44.3697500	50.16000	53.4100	57.28000	67.110750	1.	
001682	2600								
C[2,1]	45.449044	5.12170905	34.8597500	42.12000	45.6700	49.01000	54.920000	1.	
001453	3600								
C[2,2]	91.258556	4.53582565	81.9000000	88.20000	91.4500	94.60000	99.070000	1.	
000999	15000								
C[3,1]	40.511111	3.09110271	34.1797500	38.58000	40.5500	42.53000	46.460000	1.	
000947	15000								
C[3,2]	95.947665	2.52574230	90.5500000	94.26000	96.1900	97.93000	99.760000	1.	
001035	15000								
...									
C[19,1]	28.743148	6.32876678	15.5394997	24.76000	29.1200	33.05000	40.160000	1.	
001463	15000								
C[19,2]	90.671262	6.05033463	77.5297500	86.58750	91.4000	95.56000	99.540000	1.	
001078	11000								
C[20,1]	36.559909	4.84658018	26.7200000	33.41000	36.5800	39.72000	46.180250	1.	
000906	15000								
C[20,2]	83.278933	4.80460593	74.3700000	80.04000	83.0200	86.26000	93.710500	1.	
000957	15000								
C[21,1]	16.444516	4.31706757	7.5599250	13.62000	16.7000	19.51000	24.170000	1.	
001025	15000								
C[21,2]	93.176995	3.02309148	87.1300000	91.21000	93.0900	95.23000	99.010000	1.	
001281	5200								
y_sim[1]	1.032867	0.22990572	1.0000000	1.00000	1.0000	1.00000	1.000000	1.	


```

001819 15000
y_sim[2]      2.964400  0.24070003  3.0000000  3.00000  3.0000  3.00000  3.000000 1.
000916 15000
y_sim[3]      2.539000  0.75479599  1.0000000  2.00000  3.0000  3.00000  3.000000 1.
001106  9600
y_sim[4]      1.055133  0.29860720  1.0000000  1.00000  1.0000  1.00000  2.000000 1.
001231 12000
y_sim[5]      1.084333  0.36354280  1.0000000  1.00000  1.0000  1.00000  3.000000 1.
001012 15000
...
y_sim[625]    1.032200  0.17653679  1.0000000  1.00000  1.0000  1.00000  2.000000 1.
001196 12000
y_sim[626]    1.992067  0.09020867  2.0000000  2.00000  2.0000  2.00000  2.000000 1.
000901 15000
y_sim[627]    2.032333  0.17726623  2.0000000  2.00000  2.0000  2.00000  3.000000 1.
000981 15000
y_sim[628]    2.426333  0.49455993  2.0000000  2.00000  2.0000  3.00000  3.000000 1.
000956 15000
y_sim[629]    2.068333  0.25285335  2.0000000  2.00000  2.0000  2.00000  3.000000 1.
000994 15000
y_sim[630]    1.099000  0.29867197  1.0000000  1.00000  1.0000  1.00000  2.000000 1.
000931 15000
deviance      592.852240 12.26409560 570.8000000 584.30000 592.2000 600.70000 618.800000 1.
001105  9700

```

Bugs model at "C:/Users/MSR07/AppData/Local/Temp/Rtmpqygmkj/model2b38292c3ad.txt", 3 chains, each with 10000 iterations (first 5000 discarded)

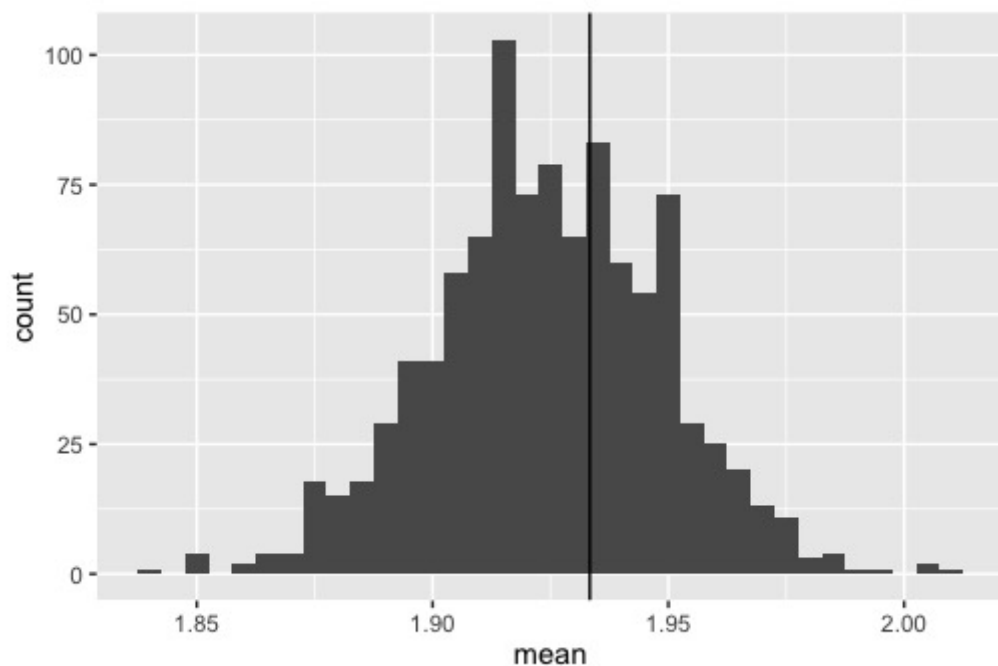


Plot

```

vote_data_plot <- data.frame(vote_data$person, vote_data$value, vote_data$vote, t(vote_j
ags_model$sims.list$y_sim[sample(1:15000, 1000), ]))
colnames(vote_data_plot)[1:3] <- c('person', 'value', 'vote')
vote_data_hist <- data.frame(mean = unlist(vote_data_plot[, -c(1:3)] %>% lapply(., mea
n)),
                             sd = unlist(vote_data_plot[, -c(1:3)] %>% lapply(., sd)))
ggplot(vote_data_hist, aes(x = mean)) + geom_histogram(binwidth = .005) + geom_vline(xin
tercept = mean(vote_data_plot$vote))

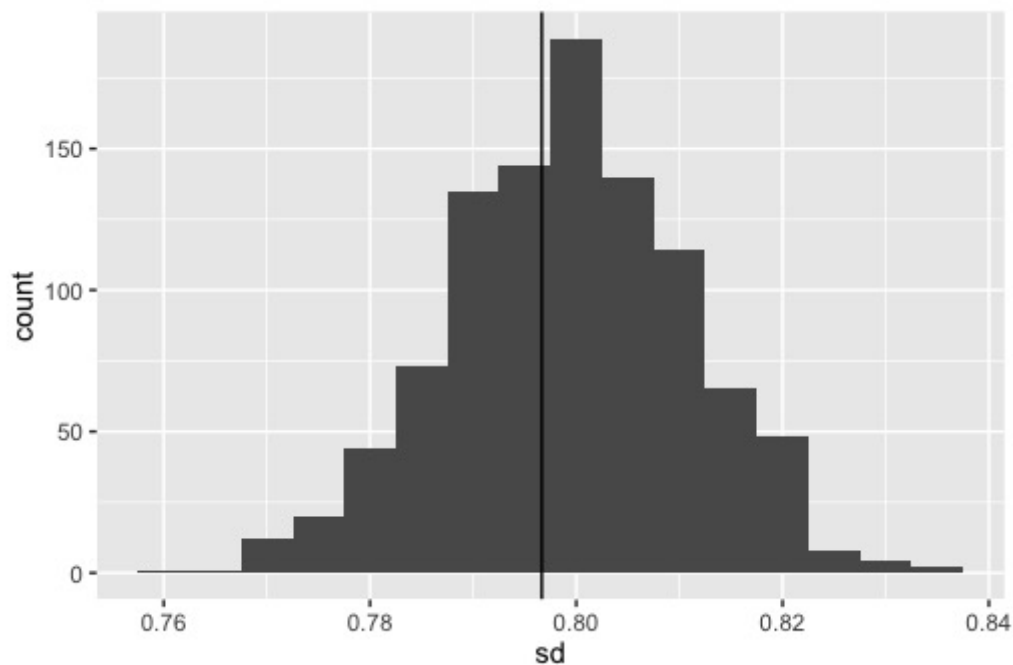
```



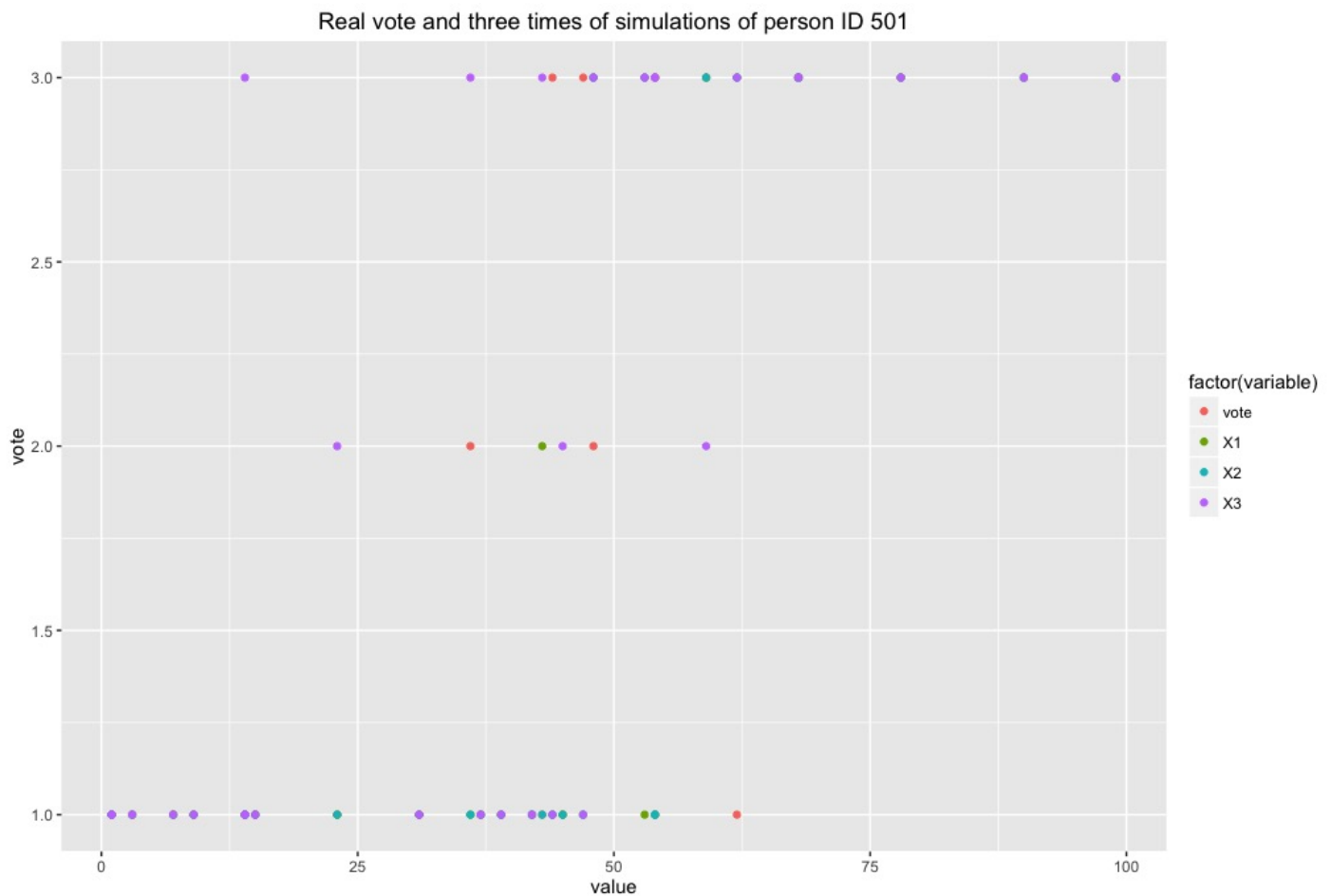
```

ggplot(vote_data_hist, aes(x = sd)) + geom_histogram(binwidth = .005) + geom_vline(xinte
rcept = sd(vote_data_plot$vote))

```



```
data_plot <- melt(vote_data_plot[, c(1:6)], id.vars = c("person", "value"))
colnames(data_plot)[4] <- "vote"
ggplot(data_plot[data_plot$person==501,], aes(x= value, y= vote, color = factor(variable))) + geom_point() + ggtitle("Actual vote and three times of simulations of person ID 501")
```



Part B

How might you expand the model to fix the problems you have found?

I use openBUGS to fit the ordered logistic regression model. The histogram plots show the predictive checks for the mean and sd of the vote. The vertical bars indicate the mean and sd of the actual data. The scatter plot shows the actual vote and the first three times of simulations of the model. Based on these plots, this model is fitted reasonable well of the actual data. In order to improve the result, I think we can add more variables into the model, like round, or increase the number of simulations.